

Scoring table:	BLOSUM62					
Gapop length:	10.0					
Gapext length:	0.5					
Searched:	100059 seqs, 36664827 residues					
Total number of hits satisfying chosen parameters:	100059					
Minimum DB seq length:	0					
Maximum DB seq length:	2000000000					
Post-processing:	Minimum Match 0% Maximum Match 100% Listing first 45 summaries					
Database :	SwissProt_39 *					
Pred.	No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.					
SUMMARIES	Description					
Result No.	Score	Query	Match	Length	DB ID	Description
1	112.5	4.1	772	1	NFL1_HUMAN	Q14494 h nuclear f
2	107	3.9	1158	1	CND1_SCHPO	Q94679 schizosacch
3	106.5	3.9	1420	1	YMBB_YEAST	Q30496 saccharomy
4	106	3.8	3206	1	POLG_PSBMV	P29152 P genome po
5	104.5	3.8	953	1	LKA3_PRSHA	P55116 pasteurella
6	104.5	3.8	4568	1	DYHC_GABEL	Q19020 caenorhabdi
7	102.5	3.7	953	1	LRKAB_PASHA	P55118 pasteurella
8	101.5	3.7	580	1	RUBA_CHLRE	Q42684 chlamydomon
9	101.5	3.7	953	1	LKA1_PAHLA	P31029 callithrix
10	101	3.7	414	1	SPYA_CALJA	Q46432 felis silve
11	100	3.6	1007	1	MA2B_FELCA	Q19069 sus scrofa
12	99.5	3.6	1181	1	YY02_METJUA	P053665 staphylococ
13	99.5	3.6	1436	1	DPO3_STAUU	P16689 felis silve
14	99	3.6	414	1	SPYA_FELCA	P052728 r poly-beta
15	99	3.6	636	1	PHBC_RHET	Q91628 xenopus lae
16	98.5	3.6	558	1	ORC2_XENLA	Q14517 homo sapien
17	98.5	3.6	4590	1	FATH_HUMAN	P91927 drosophila
18	97.5	3.5	1013	1	A60D_DROME	P27508 klebsiella
19	96.5	3.5	761	1	PQQF_KLEPN	P10193 herpes simp
20	96.5	3.5	851	1	OBP_HSW11	Q19069 escherichia
21	96	3.5	350	1	SUCA_PIG	P41842 caenorhabdi
22	96	3.5	546	1	PGMU_ECOLI	Q10147 schizosacch
23	96	3.5	787	1	Y91_LCAEL	P57700 thermoplasm
24	95	3.4	527	1	TCPB_SCHPO	Q19906 cyanidium c
25	95	3.4	665	1	ATKB_THEAC	043933 archaeoglob
26	95	3.4	1549	1	GLSF_CVACA	Q10093 schizosacch
27	94.5	3.4	614	1	Y156_ARCFU	P49025 mus musculus
28	94.5	3.4	1260	1	YAOE_SCHPO	P25984 bacillus su
29	94.5	3.4	1597	1	CTRO_MOUSE	P04114 hominidae
30	94	3.4	1071	1	CARB_BACSU	P13232 streptococc
31	94	3.4	4563	1	APB_HUMAN	Q00705 pseudorab
32	93.5	3.4	877	1	DPO1_STRPN	Q13776 schizosacch
33	93.5	3.4	1330	1	VCAP_PRVIS	

ALIGNMENTS

RESULT	1	NFL1_HUMAN	STANDARD;	PRT;	772 AA.
ID	NFL1_HUMAN	Q14494; Q12877;			
AC	Q14494; Q12877;				
DT	15-JUL-1998 (Rel. 36, Created)				
DT	15-JUL-1998 (Rel. 36, Last annotation update)				
DE	NUCLEAR FACTOR ERYTHROID 2 RELATED FACTOR 1 (NFE-E2 RELATED FACTOR 1)				
DE	(NFE2 RELATED FACTOR 1) (NUCLEAR FACTOR, ERTHROID DERIVED 2, LIKE 1)				
DE	(TRANSCRIPTION FACTOR 11) (TRANSCRIPTION FACTOR HBZ17) (TRANSCRIPTION FACTOR LCR-F1) (LOCUS CONTROL REGION-FACTOR 1).				
DE	NFE2L1 OR NRF1 (OR TCE11 OR HBZ17).				
GN					
OS	Homo sapiens (Human).				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxId:9606; [1]				
RN	SEQUENCE FROM N.A.				
RP	SEQUENCE FROM N.A.; PubMed=9095232; PubMed=8001966;				
RX	MEIDLINE=9095232; [2]				
RA	Luna L., Johnsen O., Skartlien A.H., Pedeutour F., Turc-Carel C.,				
RA	Frydz H., Kolszec A.-B.;				
RT	"Molecular cloning of a putative novel human bZIP transcription factor on chromosome 17q22."				
RT	Genomics 22:553-562(1994).				
RL					
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEIDLINE=90310069; PubMed=8036168;				
RA	Caterina J.J., Donze D., Sun C.W., Ciavatta D.J., Townes T.M.;				
RA	"Cloning and functional characterization of LCR-F1: a bZIP transcription factor that activates erythroid-specific, human globin gene expression."				
RT	RT				
RT	RT				
RL	RT				
CC	"FUNCTION: ACTIVATES ERYTHROID-SPECIFIC, GLOBIN GENE EXPRESSION"				
CC	"SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY)."				
CC	"SIMILARITY: BELONGS TO THE BZIP FAMILY, CNC SUBFAMILY."				
CC					
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CC					
DR	X77366; CAA5455; 1; -				
DR	EMBL; U08553; AAA20465; 1; -				
DR	ISNSP; P34707; ISKN.				
DR	MIM: 163200; -				
DR	InterPro; IPR01871; bZIP.				
DR	SMART; SM00338; BRIZ; 1.				
DR	PROSITE; PS00046; BZIP_BASIC; 1.				
KW	DOMAIN 125 288 ASP/GLU-RICH (ACIDIC).				
FT	DOMAIN 496 517 POLY-SER.				
FT	DNA_BIND 659 674 BASIC MOTIF.				

FT	DOMAIN	682	AA;	704	LEUCINE-ZIPPER.			
SQ	SEQUENCE	772	AA;	84703	MW;	C8688076046BEF5	CRC64;	
	Query Match	4.18;	Score	112.5;	DB 1;	Length	772;	
	Best Local Similarity	20.8%;	Pred. No.	1.7;				
	Matches	118;	Conservative	64;	Mismatches	181;	Indels	205;
						Gaps	27;	
QY	55	MSNVQEDDLQLATEVHYNPAELYTWLDSMLTDLNPPSSNAEYDLKAIPGDAILNQEA	114					
Db	83	LISQSVRALDRFQVP-----TEVNAW----LYHRDPEGS-----VSGSQPNNSGLA	123					
QY	115	LGASSNNOGGDDTYTTNKRKGCSNGVYETTATAESTRHWLVLDQENGVRVLHALIA	174					
Db	124	LESSGLQDVTPGD-----NGVRESETEQFGFE-----DLEDIG-----A	158					
QY	175	CAEVQ---KENLTVAEALVKQIGFLAVSQIGAMRKVATYF-----	212					
Db	159	VAPPVGSDLTKEIDIDLWLRQ----DIDLGAGREVDYSHRQEODVEKELRDGGEQ	213					
QY	213	-ABALARIV----RLSPSQSPIDH----RLSPSQSPIDH-----SLSDPQLQMHFYETCPYLKFKAHF	254					
Db	214	DTWAGEGAELARNLVLGETGESFPQAQPSGEDQTALESCECIRL-LEATCPFGENAEF	272					
QY	255	TAN-QAIIERAFQGKRRVHVD-----FSMSQGLQNPALMALAR-----	293					
Db	273	PADISSITAEVPSSESEPPALQNNNLSPPLTGTESPFDLQ----QWQDLMIMEMQAMEVNT	330					
QY	294	-PGGPPYVERLNGIGPAPDNFDY-LHEV---GCKLAHLAFAIHVEFEYRGFV	340					
Db	331	SASEILYSAAPPGDPPLSTNVSLAPTPINONVSLHQASLGGCSQDFLFSPEVE-----	383					
QY	341	ANTLADASMLELRPSEIESVANNSVF-----ELHKLLGR	376					
Db	384	-SLPVASSSTPLPLAPS--NSTSLNISTFGSTNLTGLFFPQLONGTANDTAGPLPDPLG-	439					
QY	377	PGALDKV-----LGVNVNIKIREPITVQEESNHNSNPIFLDRFTESLHYSTLFDSSL	427					
Db	440	-GLLDEAMLDEISLMDLATEEGFNVPQASOLEEFDSGSLSLD----SSHSSSSL-SSS	493					
QY	428	EGVPSGQDKVMSEVYLKGQICNVVACDGDRVERHETLSQWRREGSGAAHIGSNFA	487					
Db	494	EGSSSSSS-----SSSSSSSSSSSSSEEGAVGY	526					
QY	488	KOASMLLAL-FENGEGGYRVEESDGCLM	513					
Db	527	SSDSETLDLEEAEGAVGTOPEYSKFCRM	554					
RESULT	2							
CNDL_SCHPO								
ID	CNDL_SCHPO	STANDARD;						
AC	094679;							
DT	20-AUG-2001	(Rel. 40, Created)						
DT	20-AUG-2001	(Rel. 40, Last sequence update)						
DT	20-AUG-2001	(Rel. 40, Last annotation update)						
DE	CONDENSIN COMPLEX SUBUNIT 1 (P128).							
GN	CNDL OR SPBC776.13.							
OS	Schizosaccharomyces pombe (Fission yeast).							
OC	Fungi; Ascomycota; Schizosaccharomyces;							
OC	Schizosaccharomyces; Schizosaccharomyctaceae;							
OX	NCBI_TaxID=48956;							
RN	[1]	SEQUENCE FROM N.A., AND SEQUENCE OF 51.8-536; 658-667 AND 1126-1138.						
RX	MEDLINE-9412811; Pubmed-104185489;							
RA	Surani T., Yuasa T., Tomonaga T., Dohmae N., Takio K., Yanagida M.;							
RT	"Fission yeast condensin complex: essential roles of non-SMC subunits for condensation and Cdc2 phosphorylation of Cut3/SMC4."							
RL	Genes Dev. 13:2271-2283(1999).							
RN	[2]	SEQUENCE FROM N.A.						
RP	SEQUENCE FROM N.A.							
RC	STRAIN=972;							
RA	Lyne M., Rajandream M.A., Barrell B.G., Wedler H., Kutznar M.,							
RA	Wambutt R.; Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.							
RL	-1- FUNCTION: REQUIRED FOR CHROMOSOME CONDENSATION IN MITOSIS.							
CC	CC -1- SUBUNIT: PART OF THE CONDENSIN COMPLEX.							
CC	CC -1- SUBCELLULAR LOCATION: NUCLEAR, AND CYTOPLASMIC (DURING INTERPHASE).							
CC	CC -1- SIMILARITY: BELONGS TO THE CONDENSIN FAMILY.							
CC	CC -1- This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).							
CC	CC -1- EMBL: AB030212; BAA82624.1; DR EMBL; AL035263; CAA22886.1; KW Mitosis; Nuclear protein.							
SQ	SEQUENCE 1158 AA; 131323 MW; 37A7A2206830DF3D CRC64;							
Query	Match	3.9%;	Score	107;	DB 1;	Length	1158;	
Best	Local	Similarity	19.2%;	Pred.	No. 7.7;			
Matches	100;	Conservative	69;	Mismatches	155;	Indels	198;	Gaps 23;
QY	22	DGNGMDELLAVLGVKYVRSSEMAVDQAKLQELEVMMNSNQEDDLISOLATEVHYNPAELYT	81					
Db	53	DEDCHLEKPAI-----CSHFAED-----LSSSVRKVYDLSLTSNISSESAILED 95						
QY	82	WLDSMLTDLNPPSSNAEYDLKAIPGDAILNQFAIDSASSSSNQGGGDTYTINRKLCNSG	141					
Db	96	MISANATDFTVPOINLE-----TTGIAFQLTUVNLSLSSSNQ-----LS 132						
QY	142	VVENTTATPRESTRHVVLVQSOENGVRVHALL-ACAEVQKVNENLVAELVKQIGFLAVS	200					
Db	133	VIRSTSNTVYKGRKKNPNTNSNWNGISHVNALLDNLITLQKK-----LS 176						
QY	201	QIGAMRKVATYFABAELARRYRLSPSQTIDHS-----LSDTLOMHFYETCPYLKF	251					
Db	177	RWTTTSSERDMFLSLFLKPYTLMESINENIKNAFRSRLENIGLAVQFH-----226						
QY	252	AHFTANOAALEAFQGKRVHVIDSMSQGQLOWPALMQLALAQLPQQGPYVRLTGPPAPD	311					
Db	227	NHTTAET-----NIIQNIQY-----242						
QY	312	NFDYLHEVGCKLAHLAELAHVFE---YRGFVANTLADD-----ASMLELR	355					
Db	243	-FEHUSEYAADLVH----TVQFNSVTLAEGII-RTLCISLEFDNDVKGPKQVALFLVRL	297					
QY	356	PSEIESVAVNSVFEHLKLIGRPG----ATDKVIG---VNNQIRPEIFTVQEESNHNSP-	407					
Db	298	SSLIPNLCUKLQTLQVLDSESYTLRCAILEVANVLDQIHD---AQNMESVPA	353					
QY	408	-IFLDRF-----TESIHYSTLFDSLEGPSGQDKVMSVEYLQICNYVA 452						
Db	354	TVQSLMDLISERLIDSPYCRTKYLHVFKIFDLPKTPKRKPI-AEL-----VIR 404						
QY	453	CDGDPDRVHETLSQWRNRFGSAGFAAHIGSNAPKQASMLL 494						
Db	405	C-LQDR-----SSHVRNNAIKLFSKLL 425						
RESULT	3	YMBB_YEAST						
ID	YMBB_YEAST	STANDARD;						
AC	Q03496; Q04862;							
DT	01-NOV-1997 (Rel. 35, Created)							
DT	01-NOV-1997 (Rel. 35, Last sequence update)							
DE	01-NOV-1997 (Rel. 35, Last annotation update)							

Qy	19	EEDDGNMGDELLAV---LGKVKRSSEEMADYAQK-----LEQLEFVMMNSNQEDD	63	CC This SWISS-PROT entry is copyright. It is produced through a collaboration CC between the Swiss Institute of Bioinformatics and the EMBL outstation CC at the European Bioinformatics Institute. There are no restrictions on its CC use by non-profit institutions as long as its content is in no way CC modified and this statement is not removed. Usage by and for commercial CC entities requires a license agreement (See http://www.isb-sib.ch/announce/ CC or send an email to license@isb-sib.ch).
Db	55	DSGSNGQLQDLYKAEEELGQVEKQEGNDIKAQOTSLGT1QNVLGLTRGIVLISAPQLBK	114	CC
Qy	64	LSQL-----ATEVTHYPAELYTWLDMSMLTDLNPPSSNAEYDLKAIPGDALLNQFAI	115	CC
Db	115	LLQKNNKVQGALGSSESSIAQNSOQAQTVLVSQVSTLGSVLAGMDLD-----EAQN	165	CC
Qy	116	DSASSSNQGGGGDTYTNNKR-LKCSNGVYETT-----	147	CC
Db	166	--SDQTLTAKAGLELTNSTLNTANSVQTLDASFSEQI0SFQSKLONVKLG	214	DR DR InterPro: IPIR03593; AAA.
Db	215	ALGDKLKNIGGLDKAGLGLTIVSGLSATA---LVLAQDKDASTAKVGAGFELANQ	270	DR DR SMOTR; SK00382; AAA.
Qy	202	IGAMRK-WATYFAEAELLARRYLRLSPSQSPIDHSLSDTLOMHFYETCPYLKFAHFTANQAI	260	KW Motor protein; Microtubules; Dynein; ATP-binding; Coiled coil.
Db	271	VGNTIKAVSSYI---LAQRTAARLSSTGPVAAILASTVAL---AISPLSA-----GI	317	FT FT DOMAIN 587 652 COILED COIL (POTENTIAL).
Qy	261	LEAFQGKRUH-----	295	FT FT DOMAIN 814 844 COILED COIL (POTENTIAL).
Db	318	ADKFDRAKSLENAYAERFKKIGYEGDSLLAFYQHGTGTIDASVT-----AINTALAATAG	371	FT FT DOMAIN 1241 1274 COILED COIL (POTENTIAL).
Qy	296	G-----PPVFRLIGTGIPAPDNFDYHEVGCKLAAEIAH--VFEF-----	335	FT FT DOMAIN 1324 1340 COILED COIL (POTENTIAL).
Db	372	GVSAAAAGSVVASPVASPTALLYGIGTGVISTIILQYSKQ---AMEHVANKIHKHIVEKNNNG	429	FT FT DOMAIN 1559 1591 COILED COIL (POTENTIAL).
Qy	336	-----YRGFVANTLADDSM---LEURPSEIESYAVNSYF-----LHKLIGRPGDAIK	382	FT FT DOMAIN 1964 1992 MICROTUBULE-BINDING (POTENTIAL).
Db	430	KNYFENGYDARYLANIQDNMKFLMLN-KELOAERVIAITQQQWDSNCIDLAGTSRLGRK	488	FT FT DOMAIN 31132 3229 COILED COIL (POTENTIAL).
Qy	383	VLGVVNQNIKEKIFITVVEQESNNHNSPISLDFETTESLHY-----TLEDSLGV---	435	FT FT DOMAIN 3339 3432 COILED COIL (POTENTIAL).
Db	489	VL-----SGKAYVDAFFEOHLKADKLYQDLSAKGIIIDVSNTEGA	528	FT FT DOMAIN 4359 4386 COILED COIL (POTENTIAL).
Qy	436	KVMSEVYLGKQICINVCADGPDYERHET-----LSQWRNRFGA-----	475	FT FT DOMAIN 1865 1872 ATP (POTENTIAL).
Db	529	KTOHILFR----TPLLTPTEKRVERTQTKYKEYITKLHNIRVDSWQIKDGAASSTFDLT	583	FT FT DOMAIN 2163 2170 ATP (POTENTIAL).
Qy	476	-----GFAAAHIGNSNAF--KOASMILL-----FNGGGGY-RVEESEGD	510	FT FT DOMAIN 2537 2544 ATP (POTENTIAL).
Db	584	NVQRIGVELDH-AENVKTKETKIVATLGDDNVFVSGGTIDGGEGYDRHYSRG	641	FT FT DOMAIN 2880 2887 ATP (POTENTIAL).
RESULT	6	DYHC_CAEEL	5	DB 028E52684F81676 MW; 028E52684F81676 CRC64;
DB	10	SEQUENCE FROM N.A.	1	DR 3.8% Score 104.5; DB 1; Length 4568;
DB	11	STRAIN=BRISTOL N2;	1	DR Best Local Similarity 22.28; Pred. No. 87;
DB	12	MEDLINE=9614101; PubMed=8674131;	1	DR Matches 105; Conservative 47; Mismatches 145; Indels 177; Gaps 24;
Qy	113	FADIDASSSNQGGGDTYTNNKRIKCSNSGVETTATATESTREVILDSQENSVRVH--	170	DR Query Match 3.8% Score 104.5; DB 1; Length 4568;
Db	3644	FTVTSSSLASQ-----	1	DR Best Local Similarity 22.28; Pred. No. 87;
Db	3836	NTLADDASMLLRPSEIESYAVNSYFELHKKLGR-----	1	DR Matches 105; Conservative 47; Mismatches 145; Indels 177; Gaps 24;
Qy	171	-AUJACAEAVQKENL---TVAEALVKQIGFLA-VSQIGAMRKVATYFAEALARRYRLSP	225	DR Query Match 3.8% Score 104.5; DB 1; Length 4568;
Db	3690	KALLAALNNSKGKTLDDNSVIETLEKLNNEAAVQKSAETDYMAYEDDAVRAQYQLST	3749	DR Best Local Similarity 22.28; Pred. No. 87;
Qy	226	SQSPIDHSLSDTLQMF--YETCPYLK-FAHTFQANQALEAFQGKRVHVIDFSMSQGL	281	DR Matches 105; Conservative 47; Mismatches 145; Indels 177; Gaps 24;
Db	3750	ACSHYYHTLQLNLTHFLYHSLDFLWTFTHVLTKPELSSSTDYAKRLRLITTSLSFQ--	3807	DR Query Match 3.8% Score 104.5; DB 1; Length 4568;
Qy	282	QWPALMAALRPQGPVERLTIQGPAPDNFDYLHEVGKLAHLAEATHVEFYEGRFVA	341	DR Best Local Similarity 22.28; Pred. No. 87;
Db	3808	-----TVFRRVSRG-----	1	DR Matches 105; Conservative 47; Mismatches 145; Indels 177; Gaps 24;
Qy	342	NTLADDASMLLRPSEIESYAVNSYFELHKKLGR-----	1	DR Query Match 3.8% Score 104.5; DB 1; Length 4568;
Db	3836	-----SNPAPAYEQHQFDL--LIGRSRDEVAKNDEADSTIPGGIDFLVEN	3878	DR Best Local Similarity 22.28; Pred. No. 87;
Qy	382	-----KVLGVVNVQIKPEITVVEQES-----RHN-----	1	DR Matches 105; Conservative 47; Mismatches 145; Indels 177; Gaps 24;
Db	3879	KKSTAKARKVYGFEN-----VF AHLQHNSAAVTSWLTDNPESNVFVWDDADGKLSPLC	3933	DR Query Match 3.8% Score 104.5; DB 1; Length 4568;
Qy	410	L-----DRFTPSLH-YYSTLFD-----LEGVPSGQDVM-----SEV	441	DR Best Local Similarity 22.28; Pred. No. 87;
Db	3934	IMNSLIVVHALRPRDLMASAHRYVSTAFFDDHFMQ---QDKVVDLILSIVDNEVSSEP	3988	DR Matches 105; Conservative 47; Mismatches 145; Indels 177; Gaps 24;
Qy	442	YLGKQICNYYACDGPDYERHETLSQLWRNRFGSAGFAAAHIGS-NAFKQASML	494	DR Query Match 3.8% Score 104.5; DB 1; Length 4568;
Db	3989	VL---LCSATGYDASGK1---EDLAVETNR---QLSTAIGSAEGPNQADSAL	4032	DR Best Local Similarity 22.28; Pred. No. 87;
RESULT	7	LKAB_PASHA	7	DT ID LKAB_PASHA STANDARD PRT; 953 AA.
DB	11	SEQUENCE FROM N.A.	1	DT ID LKAB_PASHA STANDARD PRT; 953 AA.
DB	12	AC AC 01-OCT-1996 (Rel. 34, Created)	1	DT ID LKAB_PASHA STANDARD PRT; 953 AA.
DB	13	DT DT 01-OCT-1996 (Rel. 34, Last sequence update)	1	DT ID LKAB_PASHA STANDARD PRT; 953 AA.
DB	14	OS OS 30-MAY-2000 (Rel. 39, Last annotation update)	1	DT ID LKAB_PASHA STANDARD PRT; 953 AA.
DB	15	OC OC "Genomic structure of a cytoplasmic dynein heavy chain gene from the nematode <i>Caenorhabditis elegans</i> ."	1	DT ID LKAB_PASHA STANDARD PRT; 953 AA.
DB	16	DE DE FUNCTION: DYNEIN HAS ATPASE ACTIVITY. CYTOPLASMIC DYNEIN ACTS AS A MOTOR FOR THE INTRACELLULAR RETROGRADE MOTILITY OF VESICLES AND ORGANELLES ALONG MICROTUBULES.	1	DT ID LKAB_PASHA STANDARD PRT; 953 AA.
DB	17	RA RA -!- SUBUNIT: CONSISTS OF AT LEAST TWO HEAVY CHAINS AND A NUMBER OF INTERMEDIATE AND LIGHT CHAINS.	1	DT ID LKAB_PASHA STANDARD PRT; 953 AA.
DB	18	CC CC -!- FUNCTION: DYNEIN HAS ATPASE ACTIVITY. CYTOPLASMIC DYNEIN ACTS AS A SUBUNIT: CONSISTS OF AT LEAST TWO HEAVY CHAINS AND A NUMBER OF INTERMEDIATE AND LIGHT CHAINS.	1	DT ID LKAB_PASHA STANDARD PRT; 953 AA.
DB	19	CC CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.	1	DT ID LKAB_PASHA STANDARD PRT; 953 AA.
DB	20	CC CC -!- SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY.	1	DT ID LKAB_PASHA STANDARD PRT; 953 AA.

DE	LEUKOTOXIN FROM SEROTYPE A11.	QY	155 HVVLYDSEQENGVRVYHALLACAEEAVQKENLTVAE--ALVKQIGF--LAVSQIGAMRK-	207
GN	LkTA.	Db	222 GLSGFDKTSIGLSDVYSGUSSGATA--LYLAUKNASTSRKVAGFELANOVYGNITKA	277
OS	Pasteurella haemolytica.	Qy	208 VATYFAEALARRYLRLSPSOSPIDSLSLDTQMHFYETCPYL--KFAHTPANOQTL	261
OC	Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;	Db	278 VSSYY--LAQRVAGLSSSTGPVALIATVSL--AISPLAFAGIAKDKNHAKSLESVA	331
OX	Mannheimia.	Qy	262 EAF-----QGKKRKHVIDFSMSOGLOQWPAALRPGG-----P	297
RN	[1]	Qy	262 EAF-----QGKKRKHVIDFSMSOGLOQWPAALRPGG-----P	297
RP	SEQUENCE FROM N_A.	Db	332 ERFKLKGYDDGNLIAEYQRTGTIDRSVT-----AINTALAAATAGYSAGGRGVIASD	385
RC	STRAIN=SEROTYPE A11;	Qy	298 PVERLTGIGPPAPDNFDLYHEVGCKLAAHLAEAH--VEFE-----YRGFVENTLA	345
FX	MEDLINE=9041617; PubMed=8225575;	Qy	386 TALIVSPTGIVSITLQLYSRQ--AMFEHVANKTKEWKNHKNKFENGYDARYIA	443
RA	Burrows L.,,, Olah-Winfield E., Lo R.Y.C.;	Db	346 DLDASM--LELRSEIEEVAVNSVFE---LHKLLRPGDAKDVLYVNQIKPEIFT	396
RR	"Molecular analysis of the leukotoxin determinants from <i>Pasteurella</i> haemolytica serotypes 1 to 16."	Db	444 NLQDNMKFLINLN_KELQNEVRTAITQQWDNNNGDLAITSRLGEKVL-----	490
RR	haemolytica serotypes 1 to 16."	Qy	397 VVEQESNHNSPIFLDRFTESLHHYS--TFLDSLEGV---PSGQDKWVSEVYLGQICN	449
RL	Infect. Immun. 61:5001-5007 (1993).	Db	491 -----SGKAYVDAFEEGKHLADKLVOLDSANGIDVNSNSGKAKTQDILFR-----T	537
-!- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY DEFINED.	CC	Qy	450 VVACDGDPDRVERHET-----LSQWNRFGSA-----GFAAAHIG	483
-!- SUBCELLULAR LOCATION: SECRETED.	CC	Db	538 PLNPGTDDRERVOTKYEYITKUNINRVDWKLTGAAASSTFDLTVVQRIGFIELDNAG	597
-!- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING CC POLY(L-LYSINE).	CC	Qy	484 S-NAFKQASMLLA-----FNGGEGY-RVEESDG	510
-!- DOMAIN, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC ACTIVITY.	CC	Db	598 NVTKTKEKTRIVAKUGAGDDNVFVGSGTTEDGGGYDVRHYHSRG	641
-!- SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.	CC	RESULT 8		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	RUBA_CHLRE	STANDARD;	PRT;
CC	EMBL; U01215; AAB36689.;	ID	RUBA_CHLRE	580 AA.
CC	DR	AC	042694;	
CC	InterPro; IPR001343; HemLysn_Ca_bind.	DT	01-Nov-1997 (Rel. 35, Created)	
CC	DR	DT	01-Nov-1997 (Rel. 35, Last sequence update)	
CC	DR	DR	01-Nov-1997 (Rel. 35, Last annotation update)	
CC	PFam; PF00353; hemoLysinCaBind; 1.	DE	RUBISCO SUBUNIT BINDING PROTEIN ALPHA SUBUNIT PRECURSOR (60 kDa CHAPERONIN ALPHA SUBUNIT) (CPN-60 ALPHA).	
CC	PRINTS; PR00313; CABNDNGRPT.	DE	Chlamydomonas reinhardtii.	
CC	DR	OS	Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales; Chlamydomonidae; Chlamydomonas.	
CC	PROSITE; PS00330; HEMOLYSIN_CALCIUM; 4.	OC	NCB_TaxID=3055;	
CC	KW	OX	[1]	
CC	Transmembrane; Lipoprotein; Palmitate.	RN	SEQUENCE FROM N.A.	
CC	FT	RP	MEDLINE=5284339; PubMed=77666872;	
CC	TRANSEM	AC	Thompson M.D., Paavola C.D., Lenvik T.R., Gantt J.S.;	
CC	FT	DT	RT "Chlamydomonas transcripts encoding three divergent plastid chaperonins are heat-inducible.";	
CC	TRANSEM	DE	Plant Mol. Biol. 27:1031-1035(1995).	
CC	FT	RA	CC - FUNCTION: THIS PROTEIN BINDS RUBISCO SMALL AND LARGE SUBUNITS AND IS IMPLICATED IN THE ASSEMBLY OF THE ENZYME OLIGOMER.	
CC	POTENTIAL.	CC	CC - SUBUNIT: OLIGOMER OF PROBABLY SIX ALPHA AND SIX BETA SUBUNITS.	
CC	POTENTIAL.	CC	CC - SUBCELLULAR LOCATION: CHLOROPLAST.	
CC	POTENTIAL.	CC	CC - INDUCTION: BY HEAT SHOCK.	
CC	POTENTIAL.	CC	CC - MISCELLANEOUS: THIS PROTEIN SHOWS ATPASE ACTIVITY.	
CC	POTENTIAL.	CC	CC - SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.	
CC		CC		
CC		CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	
CC		CC	EMBL; L27472; AAA98642.;	
CC		DR	HSSP; P05139; IGRL.	
CC		DR	InterPro; IPR001844; Chaperonins_cpn60.	
CC		DR	InterPro; IPR002423; TCP1_cpn60.	
QY	19 EDDGNGMDLFLAV--LGKYKVRSEEMDAVK-----LEOLEVMMSVQEDD	63		
DB	: : : : : : : : : : : : : : : : :	55 DTERKNGDQDVKAAEELGIVQEKEENJAKAQTSLGTIONVGLTGERIVSAPQDK	114	
QY	64 LSQALATEVTHYNPAELYWLDMSMTDNPSSNAEYDLKAIPG-DAILNOFAIDSASS	121		
DB	: : : : : : : : : : : : : : : :	115 LLQKTKVQGQAIQSSE-----NLTKGFSNAKTVLSQIOLSILGSVLAGMOLDEAQK	164	
QY	122 NOGGGGDTTPTRKUKCSNGVVER-----DATAEST	154		
DB	: : : : : : : : : : : : : : :	165 N---SNELTIAKAGHETLNTSLIENIANSVTKLDAFGDQINQLGSKLQNWKGLSSLGDKL	221	

DR	Pfam; PF00118; cpn60_TCPI_1;	RA	Highlander S.K., Chidambaram M., Engler M.J., Weinstock G.M.;
DR	PRINTS; PRO0298; CHAPERONIN60.	RT	"DNA sequence of the Pasteurella haemolytica leukotoxin gene cluster.";
DR	PROSITE; PRO0304; TCOMPLEXTCPI.	RT	DNA 8.15-28(1989).
DR	PROSITE; PS00296; CHAPERONINS_CPN60_1.	RL	[3]
KW	Chaperone; ATP-binding; Chloroplast; CHLOROPLAST (PROTENTIAL); RUBISCO SUBUNIT BINDING-PROTEIN ALPHA	RN	SEQUENCE OF 884-953 FROM N.A.
TT	TRANSIT ?	RP	STRAIN-SEROTYPE A1 / BHL101.
TT	CHAIN ?	RC	MEDLINE=9026888; Published=2185213;
TT	SUBUNIT ?	RX	Highlander S.K., Engler M.J., Weinstock G.M.;
SEQUENCE	580 AA; 61863 MW; 16FD34B115E706F7 CRC64;	RT	"Nucleotide sequence of the Pasteurella haemolytica Leukotoxin.";
SO		RL	J. Bacteriol. 172:2343-2350(1990).
		CC	-: FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY DEFINED.
		CC	-: SUBCELLULAR LOCATION: SECRETED.
		CC	-: DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC ACTIVITY.
		CC	-: DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE INVOLVED IN PORE FORMATION BY THE CYTOXIN (BY SIMILARITY).
		CC	-: PIM: PALMITOYLATED BY LKTC. THE TOXIN ONLY BECOMES ACTIVE WHEN MODIFIED (BY SIMILARITY).
		CC	-: SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
		CC	--
Y	Query Match 3.7%; Score 101.5; DB 1; Length 580; Best Local Similarity 21.7%; Pred. No. 7.1; Gaps 24; Matches 100; Conservative 45; Mismatches 129; Indels 187; Gaps 24;	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation of the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announcements or send an email to license@isb-sib.ch).
Y	65 SOLATEVTYHNPALTYWLDSMLTDLNPPS-----SNAEV-----DLKAIPG-DAIL 110	DR	EMBL; M20730; AAA25520.1; .
Db	126 SYLAREMHHG-----LSQVTAGNPPIAKVKGKLDKTAIVAKLKEHAKPVKGDDIK 178	DR	EMBL; M24197; AAA25543.1; .
Y	111 NQFAIDSASSNQGGGDTTYTNKRLKCNSNV-----VETTAAV-----149	DR	PTR; S29516; S29516.
Db	179 N--VATISANDNAIGEMADALDKVGNSNVLSETNSNSETVVEVQEGERIDRGYISP 235	DR	InterPro; IPR001343; Hemolysin_ca_bind.
Y	150 -----ESTRHIVLVDSQ-----ENGVRIWHALLACAEVQKENL-----184	DR	InterPro; IPR003355; RTX_N_Pfam; PF003343; hemolysinCabinD; 1.
Db	236 QFVTNQERLRYEYDNCRVLTDQKIDAIROLIPLQEVTQRINAPLIIAENVSGEALATL 295	DR	Pfam; PF02322; RTX; 1.
Y	185 -----TVAEALYQ1QGF---LAVSQTGAMRK 207	DR	PRINTS; PRO0313; CABNNGRPT.
Db	296 VWNKLGVLNCA1KAPGFGERKSLLQDIAVITGAEFKIDLGNMKVQEAVQGVARK 355	DR	PROSITE; PS00330; HEMOLYSIN_CALCIUM; 4.
Y	208 V-----ATYEAELAAR----RIVRLSPSSP0SPIDHSLSQTLOMIFYETCFYLFKAHFETA 256	KW	Hemolysis; Toxin; Cytolytic; Cytoxin; Repeat; Calcium;
Db	356 VTVANNTTLLADAASKRDETERMIAOLKKKEAETD-SVYDEKLK-----ERIAKLSG 407	KW	Transmembrane; Lipoprotein; Palmitate; Potential.
Y	257 NOAIL----EAFQCKKRHVIVIDFMSQGLQWPAIMQALLRPGPPVFRLTGIGPPAP 310	FT	TRANSMEM 229
Db	408 GVAVKVKGAATTEAELDRKLRIED---AKNATFAAVEEGIVW--PGS-----448	FT	TRANSMEM 297
Y	311 DNFDYLHEVGCKLHIAEAATHEFEYRGFVANTLAD----LDASMLELR-PSEI--ES 361	FT	TRANSMEM 318
Db	449 -----QNLH1KSELVPFAKE-----TLEDAEKKGAD1VWKSLRAPCRLIADN 492	FT	TRANSMEM 390
Y	362 WAVNSVFELHKLLGRP----GAIDKV----LGVYNQIK 391	FT	DOMAIN 734
Db	493 AGVEGEVIVQRLGKPFEGVNAMIDKVNLNDAGVTDPAK 533	FT	REPEAT 734
		FT	REPEAT 734
		FT	REPEAT 743
		FT	REPEAT 752
		FT	REPEAT 761
		FT	REPEAT 770
		FT	REPEAT 779
		FT	CONFFLICT 409
		FT	CONFLICT 414
		FT	CONFLICT 742
		SQ	SEQUENCE 953 AA; 101996 MW; 7F93D113A118C05F CRC64;
		Query Match 3.7%; Score 101.5; DB 1; Length 953;	
		Best Local Similarity 18.8%; Pred. No. 15; Mismatches 207; Indels 221; Gaps 3	
		Matches 122; Conservative 100; MisMatches 207; Indels 221; Gaps 3	
Qy	9 KAL_PASHA STANDARD PRT; 953 AA.	Qy	19 EEDDGNGMDELLAV--LGKVRSSEMADVAQK-----LEQLEYMMNSVQYQD 63
NN	[1] D LKAL_PASHA STANDARD PRT; 953 AA.	Db	55 DTEQGNQLQDLVKAELGLIEQREFRNNTAQTSIGTQIAIGLTERGIVLQAQIDK 114
NN	[1] SEQUENCE FROM N.A.	Qy	64 LSQ-----ATETVHYNPAELTWFDSMLTDNPPSSNAEYDLKAIPGDAILNQFAI 115
NN	[1] STRAIN=SEROOTYPE A1; MEDLINE=87306837; PubMed=3040588;	Db	115 LLQKTKAGQALGSAEVQNANKAKIVLGSQIOTSVLGMQDLEALQNNNS-NQHAL 171
NN	[2] "Nucleotide sequence of the leukotoxin genes of Pasteurella haemolytica A1." Infect. Immun. 55:1987-1996(1987).	Qy	116 DSASSNQGGGDTYTTNKRJKCSNGVYETT-----

Db	172	AKAG-----LELTNSLIENANSVKTLDDEFGEQTISQFSSKLQNIGLGT	215	CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
Oy	149	TAESTPRHVLVLDQSSEQNGVRVLYHALLACAEAVQKENLTVAE---ALKQIGF--LAWSQI	202	CC or send an email to license@isb-sib.ch).
Db	216	LGDKLKNIGGDKAGLGDVKLTDVSGLSDGATA---LVLDKNASTAKKVYAGGFELANQVY	271	CC
Oy	203	GAMRK-VATYFAELARLTYRLSPSQSPIDHSLSPTLOMHYETCPYL----KFAHFT	255	DR EMBL: M84414; AAA35397.1; -
Db	272	GNTIKRASSYT---LAQRVAGLSSGPVAAILASTVSL---AISPLAPAGIADKFNHAK	325	DR PIR: S24154; S24154.
Oy	256	ANQAILEAF----OGKRRVHVDFMSQGLQWPAALRPGG-----	296	DR InterPro: IPR000192; Aminotransf_class_V.
Db	326	SLESTAERFKLGVDGNLIAEYQRGTGTIDASVY-----AINTALAATAGGVSAAAG	379	DR Pfam: PF00266; aminotran_5; 1.
Oy	297	----PPVFRITGIGGPAPDNFDLHEVGCKLAIAEAIH---VEFE----YRQE	339	DR PROSITE: PS00595; AA_Transfer_CLASS_5; 1.
Db	380	SVIASPIALVSGITGVISTIQLQSKQ---AMEHVANKLNKHIVEWEKNNHGNKFENGY	437	DR KW Transferase; Aminotransferase; pyridoxal phosphate; Peroxisome;
Oy	340	VANTLADLDASM---LELRPSEIESVSKY---LHKLLGRPAIDKVYLGVVNQI	390	DR Mitochondrion; transit peptide; Alternative initiation.
Db	438	DARYLANLQDMKFLNLN KEOQERVIAITQQQWDNNIGDLAGISRGKEVKL----	490	FT TRANSIT 1 23 MITOCHONDRIAL ISOFORM.
Oy	391	KPEIIFTVVEQESNHNSPIFLDRFTESLHYS---TLFDSLEGV---PSQGDQVMSEYVL	443	FT CHAIN 24 414 SERINE- PYRUVATE AMINOTRANSFERASE,
Db	491	-----SGKAYDAFEEGKHKIAKDLVQLQDSANGIITDVNSNCKAKTOHILFR	536	FT CHAIN 23 414 SERINE- PYRUVATE AMINOTRANSFERASE,
Oy	444	GKQICRNVVAQCDPDRVERHET-----LSQWRNRFNSGA-----GF	477	FT BINDING 231 231 FOR PYROXAL PHOSPHATE (BY SIMILARITY).
Db	537	-TPLLTPGTERRVQTKYEYITKLININRVDWKITDGAASSTEDLTNVQRIGI	591	FT SEQUENCE 414 AA: 45054 MW: 604866DA42EDDE1 CRC64;
Oy	478	AAHHTGS-NFKQASMLLA-----FNGGGY-RVEESDQ	510	Query Match Score 3.78;
Db	592	ELDNAGNVTKTKEYTIAKLGELEGDDNFVFGSGTEIDGGEGYDRHYSRG	641	Best Local Similarity 21.9%; Pred. No. 4.7;
<hr/>				
RESULT 10				Matches 70; Conservative 41; Mismatches 115; Indels 94; Gaps 15;
ID SPY-CALJA		STANDARD	PRT	414 AA.
AC P31059;				
DP 01-JUL-1993 (Rel. 26, Created)				
DP 01-JUL-1993 (Rel. 26, Last sequence update)				
DT 30-MAY-2000 (Rel. 39, Last annotation update)				
DE SERINE--PYRUVATE AMINOTRANSFERASE, MITOCHONDRIAL PRECURSOR (EC 2.6.1.51) (SPT) (ALANINE--GLYOXYLATE AMINOTRANSFERASE)				
DE (EC 2.6.1.44) (AGT).				
GN AGXT OR AGT1.				
OS Callithrix jacchus (Common marmoset).				
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
CC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae;				
CC Callithrix.				
CO NCBI_TaxID=9483;				
RN [1]				
RP SEQUENCE FROM N.A.				
RX MEDLINE=92339467; PubMed=1339350;				
RA Purdie P.E., Lumb M.J., Danpure C.J.;				
RT "Molecular evolution of alanine/glyoxylate aminotransferase 1 intracellular targeting. Analysis of the marmoset and rabbit genes."				
RL Eur. J. Biochem. 207:757-766(1992).				
CC -!- FUNCTION: DUAL METABOLIC ROLES OF GLUCONEOGENESIS (IN THE MITOCHONDRIA) AND GLYOXYLATE DETOXIFICATION (IN THE PROXISOMES).				
CC -!- CATALYTIC ACTIVITY: L-SERINE + PYRUVATE = 3-HYDROXYPYRUVATE +				
CC -!- CATALYTIC ACTIVITY: L-ALANINE + GLYOXYLATE = PYRUVATE + GLYCINE.				
CC -!- COFACTOR: PYRIDOXAL PHOSPHATE				
CC -!- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX AND PEROXISOMAL.				
CC -!- SIMILARITY: BELONGS TO CLASS-V OF PYRIDOXAL-PHOSPHATE-DEPENDENT AMINOTRANSFERASES.				
CC This SWISS-PROT entry is copyright. It is produced through a collaboration with the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial				
CC use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial				
CC RELEASED DURING GLICOPOROTEIN TURNOVER (BY SIMILARITY).				
CC CC				

-!- CATALYTIC ACTIVITY: HYDROLYSIS OF TERMINAL, NON-REDUCING
 CC ALPHA-D-MANNOSE RESIDUES IN ALPHA-D-MANNOSIDES.
 CC -!- SUBCELLULAR LOCATION: LYSOSOMAL.
 CC -!- PTM: PROCESSED INTO 3 PEPTIDES OF 72 KDA, 41 KDA AND 12 KDA.
 CC -!- DISEASE: DEFECTS IN MANE ARE THE CAUSE OF LYSOSMAL ALPHA-D-MANNOSIDOSIS, A LYSOSOMAL SPORADIC DISEASE CHARACTERIZED BY ACCUMULATION OF UNBRANCHED OLIGOSACCHARIDES CHAINS.
 CC -!- SIMILARITY: BELONGS TO FAMILY 38 OF GLYCOSYL HYDROLASES.

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CC EMBL; AF010191; AAB97672.1; -.
 DR AF010192; AAB97733.1; -.
 DR InterPro; IPR005062; Glyco_hydro_38.
 DR Pfam; PF01074; Glyco_hydro_38; 1.
 KW Hydrolase; Glycoprotein; Lysosome; Zymogen; Signal.
 FT SIGNAL 1 50 BY SIMILARITY.
 FT CHAIN 51 1007 LYSOSOMAL ALPHA-MANNOSIDASE.
 SEQUENCE 1007 AA; 113230 MW; C064A8168F5DC20A CRC64;

Query Match Score 100; DB 1; Length 1007;
 Best Local Similarity 19.0%; Pred. No. 20;
 Matches 104; Conservative 80; Mismatches 185; Indels 178; Gaps 32;

Qy 74 YNPAAELYTWLDSM-----LTDLNPPSSNAEYDLKAIPGDAILNQFAIDSASSSNQQGG 127
 Db 262 YNPEPKLCW-DTCADPFVDRSPYNAE-----ELVNYP-LOLATAQ-----G 305
 Qy 128 DTYTTNKRKCSNGVVFETTAT--AESTRHVLVDSQE--NG-VRLVHALLAC-AEA 179
 Db 306 QFERTNTIIMTGSDFQYENANNMWERNLDRLLQLVNAQQQNSRNLYSTPACYLWE 365
 Qy 180 QRENNTVAEALYRQIQFIAVSQGMKRVTAFAEALARYRLSPSQSPIDHSLSLDTIO 239
 Db 366 NKRNLWTW-----VKQDDFPYAD-GPHOFWSGYFSSRPALKRY-----ERLS 407
 Qy 240 MHFYETC-----PYLKFAHTFANQALL---EAFOGKKRHVYI-DFSMSQ 279
 Db 408 YNFLQVNQLEAGPAVNGPGSGSAPLQMAVQLQHDAVSTSKHQVADDYARQL 467
 Qy 280 GLQWP-----ALMQALAIRPGGPVFRLTGIGPPAPDNFLHEVG---CKLAHLAE--- 328
 Db 468 AAGWDPCPEVLSNALA-----RLSG-----SKEDFTYCRNLNVSVCPQLSQTAKNEQV 514
 Qy 329 -----AIHVDEFYRQFV-----NTLADLDSLME-----LRISEIESVAVN 365
 Db 515 TIYNPLGRKIDMMVRPVSKHGFVVRDPNGTVPSDVILLPSDQELLFAASVPALGF- 573
 Qy 366 SVEFLHKLG-RPGA-----IDKVLGVNYQ----IKPEITIVVEOBNSHNNSPIF 409
 Db 574 SYISVSQVPGQDPFHAKPQPQRSPQRSPRSVLAQNEHTRARPDGLLIVENNDONLL 633
 Qy 410 LDRFTESLHY-----STLFDSEGV---PSGQDKYMSSEYLGKQICNYVACDGPDFVE 460
 Db 634 PVR---QAFWYVNASVGNLNLSTOVSGAYIFRPQEKPMLVMSWAQTLVKT----PLVQE 686
 Qy 461 RHETLSQWRNNGSAGRAAHGSNAFKQASMLAIFNGGGYRVEDSGQMLGHTRP 520
 Db 687 VHQNEFSAW-----CSQVRLYRGQRHLEL-----WTVGP 716
 Qy 521 LIATSAW 527
 Db 717 IPVGDGW 723

YY02_METJ A STANDARD; PRT; 1181 AA.
 ID YY02_METJA
 AC 060301;
 DR 01-NOV-1997 (Rel. 35 Created)
 DR 01-NOV-1997 (Rel. 35 Last sequence update)
 DR 20-AUG-2001 (Rel. 40 Last annotation update)
 DE HYPOTHETICAL PROTEIN MJEC502.
 GN OS Methanococcus jannaschii.
 OC Archaea: Eurarchaeota; Methanococcales; Methanococcaceae;
 OC Methanococcus;
 OX NCBI_TAXID=2190;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPRINT-JAL-1 / DSM 2661 / ATCC 43067;
 RX MEDLINE=96137999; PubMed=1688087;
 RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
 RA Sutton G.G., Blattner J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
 RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
 RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
 RA Scott J.L., Geochagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
 RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
 RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
 RA Klein H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
 RT Complete genome sequence of the methanogenic archaeon, Methanococcus
 RT jannaschii;
 RL Science 273:1058-1073(1996).
 CC -!- SIMILARITY: WEAK IN THE C-TERMINUS, TO ADENINE-SPECIFIC
 CC METHYLTRANSFERASES.
 CC -----
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 CC -----
 DR EMBL; L77119; AAC37000.1; -.
 DR TIGR; MJECCS02; -.
 DR InterPro; IPR002296; N12N6_mtfrase.
 DR PRINTS; PRO0507; N12N6MTTFASE.
 DR PROSITE; PS00992; N6_MTASE; 1.
 DR TRANSMEM 837 857 PCTENTIAL.
 SQ SEQUENCE 1181 AA; 9F961D8F8C6A4BDD CRC64;
 DR TWLSDM1TDLNPPSSNAEYDLKAIP-GDATLNFQALDSASSSNQQGGITYTNKRLKCS 139
 DR 524 SALKELLQIKKRIVYLRF-EEMDIYK---EKLGIIILNNLYGVDDIDIAVEI----AKLR 574
 Qy 24 NGMDELLAV--LGKVRSSEMADVQKLEOLEVMNSVQEDDLSQLATEVHYNPALEY 80
 Db 575 LWL-ALIENL-----DVEALKRGEVLPNIEW-----VRCG 605
 Qy 140 NGVVEETATAESTRHVLYDQSQENGVRLYHALLACEAVQKENUTVA-FALVKOIGFLA 198
 Db 606 NSLWGMDENIKQLSISYLCDNVRIMCVLEGTLIAHNSEERKKLAKAKLLEKRDGYVL 665
 Qy 199 VSQIGAMRKVATYFABALARRIYRLSPS-OSPIDHSLSDTLQMHPYETCPYLKAHF--- 254
 Db 666 DNYVEYAH-----LLVEVYRSHGLKANLKLKELDERDTSYESTPAYEIQYON 716
 Qy 255 -----TANOQALIEAFQGKKRKH-YIDFMSMSQGLQWPALMOALA1RPGGPPVFRL 302
 Db 717 GNNKKKNGKSKRNRRVREFEKLFHWKIDFG-----WIKEBGFDTIGNPPYGNL 770

Db	333	VKDPALRL-----PTVTTVA	347
DC	Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis .		
DX	NCBI_TaxID=9685;		
RN	[1]		
RN	SEQUENCE FROM N. A.		
RC	TISSUE-Live;		
RX	MEDLINE-94221011; PubMed-8169541;		
RX	Lumb M.J., Purdue P.E., Danpure C.J.; "Molecular evolution of alanine/glyoxylate aminotransferase 1 intracellular targeting. Analysis of the feline gene." ; Eur. J. Biochem. 221:53-62(1994).		
RT	-!- FUNCTION: DUAL METABOLIC ROLES OF GLUCONEOGENESIS (IN THE MITOCHONDRIA) AND GLYOXYLATE DETOXYIFICATION (IN THE PEROXISOMES).		
CC	-!- CATALYTIC ACTIVITY: L-SERINE + PYRUVATE = 3-HYDROXYBUTYRATE + L-ALANINE.		
CC	-!- CATALYTIC ACTIVITY: L-ALANINE + GLYOXYLATE = PYRUVATE + GLYCINE.		
CC	-!- COFACTOR: PRIDOXAL PHOSPHATE.		
CC	-!- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX (>90%) AND PEROXISOMAL (10%).		
CC	-!- SIMILARITY: BELONGS TO CLASS-V OF PYRIDOXAL-PHOSPHATE-DEPENDENT AMINOTRANSFERASES.		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenses@isb-sib.ch).		
CC	EMBL; X75933; CA53527; 1; "-" InterPro; IPR0192; Aminotransf_class_V.		
CC	PFAM; PF00266; aminotran5_1; PROSITE; PS00342; MICROBODIES_CTER; 1; PROSITE; PS00595; AA_TRANSPER_CLASS_5; 1.		
KW	Transfase; Aminotransferase; Pyridoxal phosphate; Peroxisome; Mitochondrion; Transit peptide; Alternative initiation.		
FT	TRANSIT_CHAIN 1 23 MITOCHONDRIAL (BY SIMILARITY).		
FT	CHAIN 24 414 SERINE--PYRUVATE AMINOTRANSFERASE,		
FT	CHAIN 23 414 MITOCHONDRIAL ISOFORM.		
FT	INIT_MET 23 23 SERINE--PYRUVATE AMINOTRANSFERASE,		
FT	BINDING SITE 231 231 SERINE--PYRUVATE AMINOTRANSFERASE, PEROXISOMAL ISOFORM.		
FT	SITE 412 414 MICROBODY TARGETING SIGNAL (BY SIMILARITY).		
SQ	SEQUENCE E 414 AA; 45507 MW; ODIBOLEOE9A19983 CRC64;		
Query Match	3.6%; Score 99; DB 1; Length 414;		
Best Local Similarity	21.9%;		
Matches	70; Conservative 43; Mismatches 113; Indels 94; Gaps 15;		
Query Match	3.6%; Score 99; DB 1; Length 636;		
Best Local Similarity	21.6%;		
Matches	80; Conservative 50; Mismatches 138; Indels 102; Gaps 1		
Query	15 MMNNEEDGNGMDELLAVLGKYVRSSSEMAVAQKLEOLEVMSNVDDDLSQL-----AT 69		
DB	233 MKMLAEDIAGKGEL-----RLRQDTMTKFAVGRDMALTPGKVIAQNDICQIQQYEAST 286		
Query	70 ETVHYNPAELYTWLSDM-LIDLNPPPS-----NAEVYDKAI 104		
FT	ACT-SITE 373 373 POTENTIAL.		
SQ	SEQUENCE 636 AA; 71935 MW; DD370C10ECC89D12 CRC64;		
Query Match	3.6%; Score 99; DB 1; Length 636;		
Best Local Similarity	21.9%;		
Matches	70; Conservative 43; Mismatches 113; Indels 94; Gaps 15;		
Query	292 LRPGGGPVFRITGIGP-----DNFDYLHEVGCKLAHLAEIAHVEFEYRGFVA 341		
Db	37 IRLPLSPTRNLRLGPSPNSLAPRVLYAGGKQNGMHHK----EMFOIMDDIKRGQJTVFQTK 93		
Query	342 NTL-----ADDASMLE-LRPSBEISAVNSVF-----ELHKLGRPG 378		
Db	94 NPLTLAISGSGHCALEAALFNLILEFPDFELGVNGIWIQQRADIGERIGARVHPMIKDPG 153		
Query	379 ---ADKVGLGVNQIKPEIITVVEQSNHNSNPFLDRTEELHYSTLF----DSLEGV 430		
Db	154 NYHTLQELEELAQHQPVLLELTQGESSSGVLPQLDGPSSVLSLSCGT 213		
Query	431 P-----SGQDKVMS-----EVYLG-KQICNVV 451		
Db	214 PTYMDQGQIDVLYSGSQKVUNSPPGTSLISTSDFAKKNKIVTRKTKEVSFLDMKVNANIW 273		
Query	452 AGDGPDRVERBET---LSQWRNRFGSGFAAHIGSNAFQKOSMILLAFNG---GEGYRVE 506		
Db	274 GCDGKPRIYHHTPVVLSLYSURESLALIAEGL-ENSWRQHREVAYLHGRQLGLQFL 332		
Query	507 ESDGCLMLGNTRPLIATSA 526		
Query	207 KVATYFFEARIRRSPQSOPDHS-----SDFLCM-----HEYFCPCVKERHTAN 257		

Db	451	LWPFVNSYLK-----GQEPLPFDLFWNADSTRMAAAANHAFLRNCYLRNA-LTN	502
Qy	258	QALEAFQGK-----RVHYIDFSMSQGLQWPAALALR-PGGPPYFRLTGIGPPA-	309
Db	503	: : : : : : : : : : : : : : : : : : : : : : : : : : : :	
Db	503	EMILD--GKRISLKDVKIPYLNLATREDHTAPAKSVFLGSRFGGKVEFVVTGSHIAG	559
Qy	310	----PDNFDY 315	
Db	560	VVNPPDKRY 569	

Search completed: May 8, 2002, 11:11:55
Job time: 215 sec